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Total number of hits satisfying chosen parameters:
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 02-Sep-2000
C;Accession: JC5964
R;Steblilk, C; de Martin, R.; Binder, B.R.; Lipp, J.
Biochem. Biophys. Res. Commun. 243, 827-832, 1998
A;Title: Cytokine induced expression of porcine inhibitor of apoptosis protein (iap)
A;Reference number: JC5964; MUID:98162622
A;Accession: JC5964
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A;Title: Suppression of apoptosis in mammalian A;Reference number: A58182; NUID:96149249
A;Accession: S68450
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                                                                                                                           A;Molecule type: DNA
A;Residues: 1-358 <STE>
A;Residues: 1-358 <STE>
A;Cross:references: GB:U79142; NID:g2957174; PIDN:AAC39171.1; PID:g2957175
C;Superfamily: RING finger homology
F;307-351/Domain: RING finger homology <RRN>
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C;Superfamily: RING finger homology
C;Reywords: apoptosis; zinc finger
F;567-611/Domain: RING finger homology <RNG>
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000
C;Accession: S68450
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S72438
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       pred. No. 3.4e-24;
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Pred. No. 1.4e-25;
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seq

length: 0 length: 2000000000

Post-processing: Minimum Match 08

Maximum Match

1008

Database

PIR\_68:\*

A 3 2 H

pir1:\*
pir2:\*
pir3:\*
pir4:\*

Sequence:

Scoring table: Perfect score:

BLOSUM62

Gapop 10.0 ,

Gapext 0

US-08-569-749-7 269

Searched:

Run on: OM protein -

Copyright

0 Gaps

0

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apoptosis inhibitor hisp-1 - human
C; Species: Homo sapiens (man)
C; Species: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000
C; Accession: S68449
R; Liston, P; Roy, N; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani, A; Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAI A; Reference number: A58182; MUID; 96149249
A; Reference number: A58182; MUID; 96149249
A; Accession: S68449
A; Accession: S68449
A; Molecule type: mRNA
A; Residues: 1-604 <LIS;
A; Cross-references: EMBL: U45878; NID: 91184315; PIDN: AAC50371.1; PID: 91184316
C; Function: Executive suppressor
                                                                                                                                                A; Description: apoptotic suppressor C; Superfamily: apoptosis inhibitor IAP homol C; Keywords: apoptosis; zinc finger C; Keywords: apoptosis; zinc finger f; 446-490/Domain: RING finger homology <RRN>
                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-161, 'C', 163-422, 'Q', 424-497 <LIS>
A; Cross-references: EMBL: 045880; NID: g1184319; |
C; Genetics:
A; Gene: 11p
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:U32974; NID:g1016687; PIDN:AAC50518.1; PID:g1016688 R;LIston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Chercon-Horvet, G.; Farahani, Nature 379, 349-353, 1996 R;LILe: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAI A:Reference number: A58182; MUID:96149249 A;Accession: 568451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               apoptosis inhibitor IAP homolog - human C;Specles: Homo sapiens (man) C;Specles: Homo sapiens (man) C;Decles: Homo sapiens (man) C;Dete: 06-bec-1996 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000 C;Accession: S69544; S68451 C;Clem, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan, M. B;Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan, M. EMBO J. 15, 2685-2694, 1986 EMBO J. 15, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-2694, 2685-
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A;Accession: S69544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 251; DB 2;
Pred. No. 2.3e-23;
1; Mismatches 2
        Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                            homolog;
        192; DB 2;
No. 3.9e-16;
                                                                                                                                                                                                                                                                                                                                                                                                          PIDN: AAC50373.1;
                                                                                                                                                                                                                            RING
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                                          Length 497
                                                                                                                                                                                                                        finger homology
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                                                                                                                                                                                                                                                                                                                                                                                                          PID:g1184320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: A58182; MUID:96149249
A;Accession: 568452
A;Strain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Genetics:
A:Genet GDB:SMA@; SMA
A:Genet: GDB:SMA@; SMA
A:Gross-references: GDB:120378; OMIM:600354; OMIM:253300
A:Cross-references: GDB:120378; OMIM:600354; OMIM:253300
A:Map position: 5q12.2-5q13
C:Keywords: apoptosis; ATP; glycoprotein; nucleotide binding; P-loop; transfc;94-110/Domain: transmembrane #status predicted <TMM1>
F:470-477/Region: nucleotide-binding motif A (P-loop)
F:479-496/Domain: transmembrane #status predicted
F:470-Momain: transmembrane #status predicted
F:470-Momain: ATP (Lys) #status predicted
F:618,632,823,923,1035/Binding site: carbohydrate (Asn) (covalent) #status |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R:ROY, N.; Mahadevan, M.S.; McLean, M.; Shutler, G.; Yaraghi, Z.; Farahani, R.; Baird d, T.O.; de Jong, P.J.; Surh, L.; Ikeda, J.E.; Korneluk, R.G.; MacKenzie, A. Cell 80, 167-178, 1995
A.Title: The gene for neuronal apoptosis inhibitory protein is partially deleted in in A:Reference number: A55478; MUID:95112344
A:Recession: A55478
A;Description: apoptotic suppressor
C;Superfamily: apoptosis inhibitor IAP homolog;
C;Kupwords: apoptosis; zinc finger
E;445-489/Domain: RING finger homology <RNG>
                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-36, 'AT', 37, 'K', 39, 'L', 41-44, 'H', 46-58, 'Q', 60-412, 'A', 414-427, 'A', 429-49
A; Cross-references: EMBL: U45881; NID: g1184313; PIDN: AAC46988.1; PID: g1184314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     apoptosis inhibitor diap - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Bpecies: Drosophila melanogaster
C;Bate: 17-7ul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Nov-2000
C;Accession: S68452; S78528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-496 <LIS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Liston, P.; Roy, N.; Tau
Nature 379, 349-353, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 02-Feb-2001
                                                                                                                                                    C; Function
                                                                                                                                                                                          A;Cross-references: FlyBase:FBgn0015247
                                                                                                                                                                                                                        C; Genetics
                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: S78528
A; Accession: S78528
                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:U45881; NID:g1184313; PIDN:AAC46988.1; PID:g1184314 R;Baird, S.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:U19251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-1232 < ROY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N; Alternate names:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 LAKAGLEYTGIKDIVQCFSCGGCLEKWQEGDDPLDDHTRCFPNCPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LARAGEYYIGPGDRVACFACGGKLSNWEPKDDAMSEHRRHFPNCPF 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LASAGLYYTGIGDQVQCFCCGGKLKNWEPCDRAWSEHRRHFPNCFF 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LARAGFYYIGPGDRVACFACGGKLSNWEPKDDAMSEHRRHFPNCPF 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Faraha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Library, January 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 149; DB Pred, No. 1.9e 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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.9e-10;
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                                                                            RING finger homology
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and

a related family of

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Graverson. Z.; Diez, E.; Gros, ...
R;Yaraghi, Z.; Diez, E.; Gros, ...
A;Title: CDNA cloning and the 5'genomic organization of Naip2,
...
Paference number: Z22179; MUID:99315342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               apoptosis inhibitor IAP homolog - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: S69545
R;Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan, M. EMBO J. 15, 2685-2694, 1996
A;Title: A conserved family of cellular genes related to the baculovirus lap gene and e A;Reference number: S69544, MJD195256286
A;Accession: S69545
                                             RESULT
T31067
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                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1447 <4VAR>
A;Cross-references: EMBL:AF102871; NID:g3860228; PID:g3860229; PIDN:AAC73002.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuronal apoptosis inhibitory protein 2 - C;Species: Mus musculus (house mouse) C;Date: 11-Jan-2000 *sequence_revision 11
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G; Superfamily: apoptosis inhibitor IAP homolog;
F;446-490/Domain: RING finger homology <RRN>
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  BIR repeat
C; Species:
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Best Local
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Best Local
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                                                                                                                                                                                                                                                       Query Macch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 LAKAGFYYLNRLDHYKCYWCNGVIAKWEKNDNAFEEHKRFFPQCP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 LAKAGFYYLNRLDHVKCVWCNGVIAKWEKNDNAFEEHKRFFPQCP
                                                                                                                              181 LSAAGEVETGKRDTVQCFSCGGCLGNWEEGDDPWKEHAKWEPKCEF 226
                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                    1 LARAGEYYIGPGDRVACFACGGKLSNWEPKDDAMSEHRRHEPNCPF 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LARAGFYYIGPGDRVACFACGGKLSNWEPKDDAMSEHRRHFPNCP 45
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  containing u
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                                                                                                                                                                                                                 Conservative
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ubiquitin-conjugating
us (house mouse)
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 140; DB 2;
Pred. No. 1.1e-09;
6; Mismatches 16
                                                                                                                                                                                                                                   Score 138; DB 2; Length 1447; Pred. No. 5.1e-09;
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No. 1.1e-09;
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                      enzyme
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                      BRUCE - mouse
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                                                               A;Cross-references: GB:L22564; NID:9456111; PIDN:AAB02610.1; PID:9456114
A;Note: authors translated the codon TGG for residue 28 as Tyr, GAC for C;Superfamily: viral apoptessi inhibitor IAP; RING finger homology F;217-261/Domain: RING finger homology <RRN>
                                                                                                                                                    A; Residues: 1-268 <BIR>
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Query Match

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Score 132;

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2

Length

268

residue

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C;Accession: T10304
R;Ahrens, C,A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
Virology 229, 381-399, 1997
A;Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedro
A;Reference number: 217011; MUID:97271300
A;Accession: T10304
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residus: 1-268 <AHR>
A;Residus: 1-268 <AHR>
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                                                                                                                                                           apoptosis-inhibiting protein - Orgyia pseudotsugata multicapsid nuclear polyhedrosis C;Spacies: Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus, OpMNPV C;Date: 15-Oct-1994 *text_change 15-Sep-2000 C;Accession: A53989
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C;Superiamily: viral apoptosis inhibitor IAP; RING finger homology
F;217-261/Domain: RING finger homology <RRN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibitor of apoptosis protein 3 - Orgyia pseudotsugata nuclear polyhedrosis virus
C:Specias: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV
C:Date: 16-Jul-1999 *sequence_revision 16-Jul-1999 *text_change 15-Sep-2000
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A;Residues: 1-4845 <HAU>
A;Residues: 1-4845 <HAU>
A;Cross-references: EMBL;Y17267; NID:93319989; PIDN:CAA76720.1; PID:93319990
A;Note: localized to the Goldi compartment and the vesicular system
C;Keywords: membrane-associated protein
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                   R;Birnbaum, M.J.; Clem, R.J.; Miller, L.K.
J. Virol. 68, 2521-2528, 1994
A;Title: An apoptosis-inhibiting gene from a nuclear polyhedrosis virus
A;Reference number: A53989; NUID:94187094
A;Accession: A53989
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A; Status: preliminary
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Best Local Similarity 45.7

Matches 21; Conservative
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Best Local Similarity
Matches 25; Conserv
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Pred. No. 5.9e
6; Mismatches
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Pred. No. 5.7e-08;
4; Mismatches 17
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probable apoptosis inhibitor - Chilo iridescent virus C;Species: Chilo iridescent virus C;Dete: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change C;Accession: T03183
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A:Molecule type: DNA
A:Residues: 1-275 <CRO>
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C; Keywords: apoptosis
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A; Residues: 1-298 <LIN>
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Matches 21; Conservative
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6; Mismatches 19;
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Pred. No. 2.7e-08;
B; Mismatches 16
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C;Superfamily: RING finger homology
F;159-202/Domain: RING finger homology <RRN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Bahr, U.; Tidona, C.A.; Darai, G.
Virus Genes 15, 235-245, 1997
A;Title: The DNA sequence of Chilo iridescent virus between the genome coordinates A;Reference number: 214834; MUID:98141693
A;Accession: T03183
                                                                                                                                                                                                                                                                                                                                                                        A; Note: MSV248
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A; Residues: 1-208 <BAH>
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Best Local Similarity
Matches 20; Conserv
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Best Local Similarity
37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 LSRAGETYLNIGDQVQCFYCDLKLKEWKRSDNPFEEHKKHTQDLKINCLF 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15
                                                            1 LARAGFYYIGPGDRVACFACGGKLSNWEPKDDAMSEHRRHFPNCPF 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LARAGEYYIGPGDRVACFACGGKLSNWEPKDDAMSEHRRHFP----NCPF 46
LCEAGFFYTNIGDITVCFNCGLKIKNWLYYNDPWIEHSKWSPNCNY 82
                                                                                                                                                                Conservative
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Pred. No. 3.4e-07
7; Mismatches 1:
                                                                                                                                                           Score 111; DB
Pred. No. 1.4e-
5; Mismatches
                                                                                                                                            8 2;
1-06;
21;
                                                                                                                                                                                                                                           Length 150
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